

Figure 3–figure supplement 2

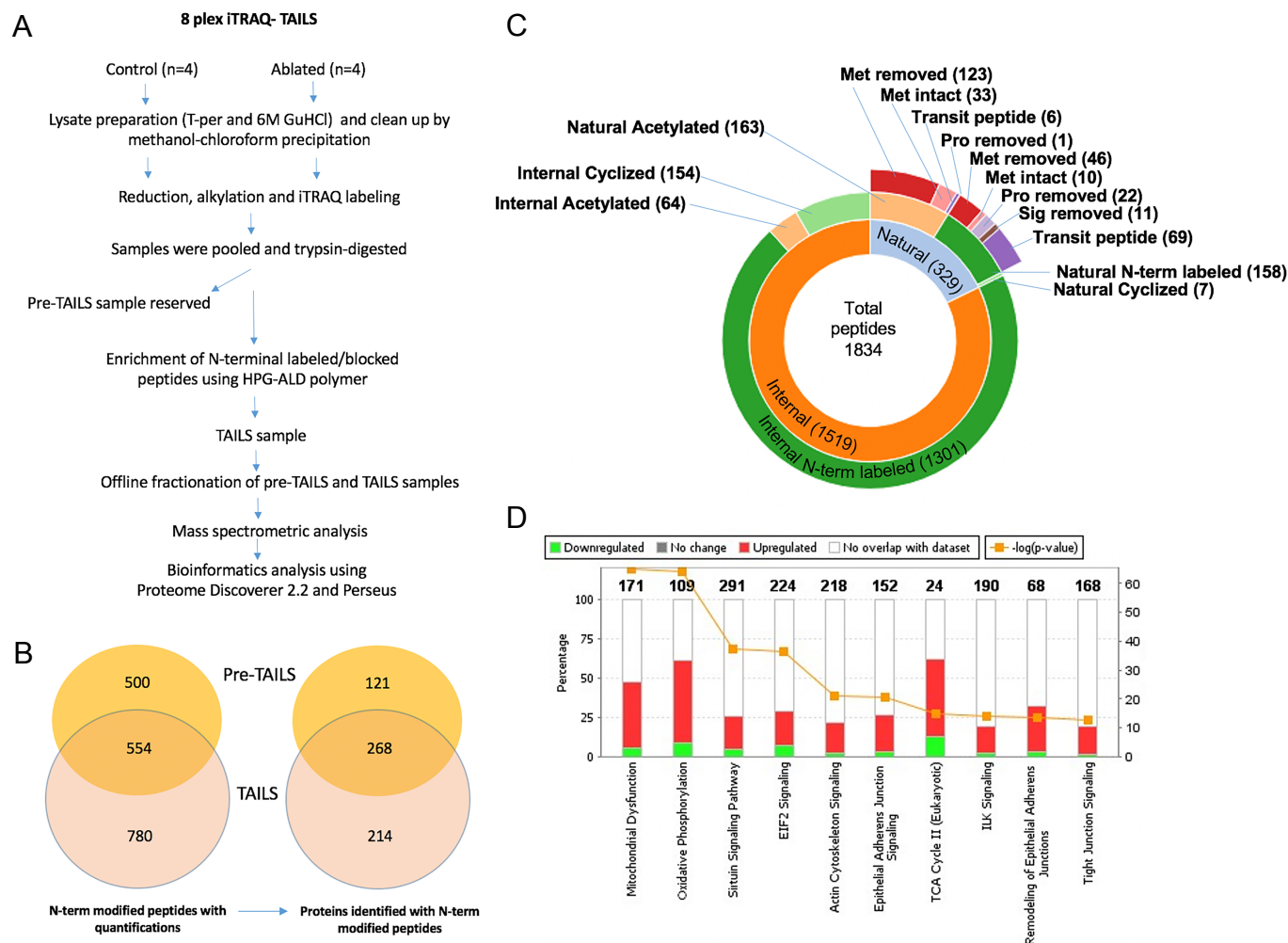


Figure 3–figure supplement 2. N-Terminomics of whole ventricle tissue. (A) Proteolytic changes were determined by 8-plex iTRAQ-TAILS N-terminomics on whole heart tissue using the illustrated workflow. (B) A Venn diagram illustrating the overall yield of Nterminally blocked/labeled peptides from the pre-TAILS and TAILS samples and the corresponding number of proteins they originated from. Of 1834 N-terminally blocked/labeled peptides, 780 were identified exclusively in TAILS demonstrating the value of excluding unblocked tryptic peptides by HPG-ALD polymer. (C) Sunburst plot displaying all N-termini from fibroblast-ablated and control ventricles. The plot shows the distribution of blocked natural N-termini and internal N-termini in the innermost ring. The middle ring shows that the majority of internal N-termini were experimentally labeled with iTRAQ, whereas only a minority were acetylated or cyclized, contrasting with natural Ntermini. The outermost ring indicates the origins of the natural N-termini. Met: methionine, Pro: propeptide, Sig: signal peptide. (D) Pathway analysis of the N-terminome differences showing the top 10 canonical pathways differentially affected by fibroblast-ablation. Control: n = 3; ablated: n=3.